1646

RAW SEQUENCE LISTING   DATE: 07/18/2000
PATENT APPLICATION: US/09/096,500A   TIME: 13:35:55

Input Set : A:\P1110P1.txt
Output Set: N:\CRF3\07182000\I096500A.raw

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 3 <110> APPLICANT: Ashkenazi, Avi J.
 4         Baker, Kevin P.
 5         Chuntharapai, Anan
 6         Gurney, Austin
 7         Kim, Kyung Jin
 8         Wood, William I.
10 <120> TITLE OF INVENTION: Apo-2DcR
12 <130> FILE REFERENCE: P1110P1
14 <140> CURRENT APPLICATION NUMBER: US 09/096,500A
15 <141> CURRENT FILING DATE: 1998-06-12
17 <150> PRIOR APPLICATION NUMBER: US 60/049,911
18 <151> PRIOR FILING DATE: 1997-06-18
20 <160> NUMBER OF SEQ ID NOS: 17
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 259
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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29   1               5                  10                  15
31 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
32                  20                  25                  30
34 Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
35                  35                  40                  45
37 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
38                  50                  55                  60
40 Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
41                  65                  70                  75
43 Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
44                  80                  85                  90
46 Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
47                  95                 100                 105
49 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
50                 110                 115                 120
52 Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
53                 125                 130                 135
55 Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
56                 140                 145                 150
58 Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
59                 155                 160                 165
61 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
62                 170                 175                 180
64 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
65                 185                 190                 195
67 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
68                 200                 205                 210
70 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/096,500A

DATE: 07/18/2000
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Input Set : A:\P1110P1.txt
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71                   215                   220                   225
73  Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
74                   230                   235                   240
76  Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
77                   245                   250                   255
79  Ile Val Phe Val
82  <210> SEQ ID NO: 2
83  <211> LENGTH: 1180
84  <212> TYPE: DNA
85  <213> ORGANISM: Homo sapiens
87  <220> FEATURE:
88  <221> NAME/KEY: CDS
89  <222> LOCATION: (193) . . . (969)
90  <223> OTHER INFORMATION:
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93   gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag 50
95   atttttggga gtttgaccag agatgcaagg ggtgaaggag cgcttcctac 100
97   cgttagggaa ctctggggac agagcgcccc ggccgcctga tggccgaggc 150
99   agggtgcgac ccaggaccca ggacggcgtc gggaaccata cc  atg 195
100                                                     Met
101                                                      1
103  gcc cgg atc ccc aag acc cta aag ttc gtc gtc gtc atc 234
104  Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile
105              5                   10
107  gtc gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc 273
108  Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr
109   15                  20                  25
111  act gcc cgg cag gag gaa gtt ccc cag cag aca gtg gcc 312
112  Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
113          30                  35                  40
115  cca cag caa cag agg cac agc ttc aag ggg gag gag tgt 351
116  Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
117              45                  50
119  cca gca gga tct cat aga tca gaa cat act gga gcc tgt 390
120  Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
121      55                  60                  65
123  aac ccg tgc aca gag ggt gtg gat tac acc aac gct tcc 429
124  Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
125                  70                  75
127  aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa 468
128  Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
129   80                  85                  90
131  tca gat caa aaa cat aaa agt tcc tgc acc atg acc aga 507
132  Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
133          95                  100                 105
135  gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cgg aat 546
136  Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn
137                  110                 115
139  gaa aac tcc cca gag atg tgc cgg aag tgt agc agg tgc 585
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140  Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
141      120                 125                 130
143  cct agt ggg gaa gtc caa gtc agt aat tgt acg tcc tgg 624
144  Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
145              135                 140
147  gat gat atc cag tgt gtt gaa gaa ttt ggt gcc aat gcc 663
148  Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
149  145                 150                 155
151  act gtg gaa acc cca gct gct gaa gag aca atg aac acc 702
152  Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
153              160                 165                 170
155  agc ccg ggg act cct gcc cca gct gct gaa gag aca atg 741
156  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
157                  175                 180
159  aac acc agc cca ggg act cct gcc cca gct gct gaa gag 780
160  Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
161          185                 190                 195
163  aca atg acc acc agc ccg ggg act cct gcc cca gct gct 819
164  Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
165                  200                 205
167  gaa gag aca atg acc acc agc ccg ggg act cct gcc cca 858
168  Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
169  210                 215                 220
171  gct gct gaa gag aca atg acc acc agc ccg ggg act cct 897
172  Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
173              225                 230                 235
175  gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 936
176  Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
177                  240                 245
179  ata gtt cta att gtg ctt ctg att gtg ttt gtt t 970
180  Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
W--> 181     250                 255                 259
183  gaaagacttc actgtggaag aaattccttc cttacctgaa aggttcaggt 1020
185  aggcgctggc tgagggcggg gggcgctgga cactctctgc cctgcctccc 1070
187  tctgctgtgt tcccacagac agaaacgcct gccctgccc  caaaaaaaaa 1120
189  aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1170
191  aaaaaaaaaa 1180
193  <210> SEQ ID NO: 3
194  <211> LENGTH: 299
195  <212> TYPE: PRT
196  <213> ORGANISM: Homo sapiens
198  <400> SEQUENCE: 3
199  Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
200  1               5                  10                  15
202  Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
203                  20                  25                  30
205  Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
206                  35                  40                  45
208  Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
```

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209                   50                  55                  60
211  Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
212                  ·65                  70                  75
214  Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
215                   80                  85                  90
217  Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
218                   95                 100                 105
220  Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
221                  110                 115                 120
223  Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
224                  125                 130                 135
226  Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
227                  140                 145                 150
229  Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
230                  155                 160                 165 .
232  Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn
233                  170                 175                 180
235  Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala
236                  185                 190                 195
238  Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
239                  200                 205                 210
241  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr
242                  215                 220                 225
244  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
245                  230                 235                 240
247  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
248                  245                 250                 255
250  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
251                  260                 265                 270
253  Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile
254                  275                 280                 285
256  Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
257                  290                 295
259  <210> SEQ ID NO: 4
260  <211> LENGTH: 1180
261  <212> TYPE: DNA
262  <213> ORGANISM: Homo sapiens
264  <220> FEATURE:
265  <221> NAME/KEY: CDS
266  <222> LOCATION: (73) . . . (969)
267  <223> OTHER INFORMATION:
269  <220> FEATURE:
270  <221> NAME/KEY: sig_peptide ·
271  <222> LOCATION: (73) . . . (194)
272  <223> OTHER INFORMATION:
274  <400> SEQUENCE: 4
275  gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag 50
277  atttttggga gtttgaccag ag   atg caa ggg gtg aag gag 90
278                           Met Gln Gly Val Lys Glu
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                    RAW SEQUENCE LISTING            DATE: 07/18/2000
                    PATENT APPLICATION:  US/09/096,500A    TIME: 13:35:55

                    Input Set : A:\P1110P1.txt
                    Output Set: N:\CRF3\07182000\I096500A.raw

279                             -40                     -35
281    cgc ttc cta ccg tta ggg aac tct ggg gac aga gcg ccc 129
282    Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
283                        -30                     -25
285    cgg ccg cct gat ggc cga ggc agg gtg cga ccc agg acc 168
286    Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
287        -20                     -15                 -10
289    cag gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc 207
290    Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
291                     -5                  1               5
293    aag acc cta aag ttc gtc gtc gtc atc gtc gcg gtc ctg 246
294    Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
295                         10                  15
297    ctg cca gtc cta gct tac tct gcc acc act gcc cgg cag 285
298    Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
299        20                      25                  30
301    gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag 324
302    Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
303                     35                  40
305    agg cac agc ttc aag ggg gag gag tgt cca gca gga tct 363
306    Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
307    45                      50                  55
309    cat aga tca gaa cat act gga gcc tgt aac ccg tgc aca 402
310    His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
311                     60                  65                  70
313    gag ggt gtg gat tac acc aac gct tcc aac aat gaa cct 441
314    Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
315                     75                  80
317    tct tgc ttc cca tgt aca gtt tgt aaa tca gat caa aaa 480
318    Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
319        85                      90                  95
321    cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt 519
322    His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
323                     100                 105
325    cag tgt aaa gaa ggc acc ttc cgg aat gaa aac tcc cca 558
326    Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
327    110                     115                 120
329    gag atg tgc cgg aag tgt agc agg tgc cct agt ggg gaa 597
330    Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
331                     125                 130                 135
333    gtc caa gtc agt aat tgt acg tcc tgg gat gat atc cag 636
334    Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
335                     140                 145
337    tgt gtt gaa gaa ttt ggt gcc aat gcc act gtg gaa acc 675
338    Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
339        150                     155                 160
341    cca gct gct gaa gag aca atg aac acc agc ccg ggg act 714
342    Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
343                     165                 170
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 07/18/2000
PATENT APPLICATION: US/09/096,500A   TIME: 13:35:56

Input Set : A:\P1110P1.txt
Output Set: N:\CRF3\07182000\I096500A.raw

L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11